



SEQUENCE LISTING

RECEIVED
JUN 28 2002
TECH CENTER 1600/2900

<110> German, Ira
Welch, Alice

<120> BETA-CAP73 CONTROL OF NORMAL AND
ABNORMAL CELL MIGRATION

<130> TUI-001CP

<140> US 09/750,590

<141> 2000-12-28

<150> 60/170,182

<151> 1999-12-10

<150> 09/733,818

<151> 2000-12-08

<160> 25

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 4730

<212> DNA

<213> Bos taurus

<220>

<221> CDS

<222> (392) ... (4597)

<400> 1

```

cagtgttgag gcggcaggat gtagagtgcgt gttcaagctt tccagtggag tccccgaaaa 60
gggaaggcag agaaagacat cttctaaata acaaatagga ggagttacag tacctgactt 120
ggggctgctc ttaatcaagt gctgccgctg caaggaagat aattttcaag cgttatgaag 180
gcggagaagg attccgaaga cgaagaaaat atccttagag atccaagcta agtgtagtgc 240
agcatgaaga ttgcagaaca ggaagagttc taagaagaag gactgagtca ctagttagga 300
gtctctctga gggctggcct tgtgagccac agtgatttgt aacttaatgc gaactaattt 360
gctgttagca acaagaaact aaatcctgtc t atg atg agc tgt tgg ttt tct 412
                                Met Met Ser Cys Trp Phe Ser
                                1                               5

```

```

tgt gct cct aag aac aga caa gca gca gat tgg aac aaa tac gat gac 460
Cys Ala Pro Lys Asn Arg Gln Ala Ala Asp Trp Asn Lys Tyr Asp Asp
          10                      15                      20

```

```

cga ttg atg aga gca gca gaa agg gga gat gta gaa aaa gtg tcc tca 508
Arg Leu Met Arg Ala Ala Glu Arg Gly Asp Val Glu Lys Val Ser Ser
          25                      30                      35

```

```

atc ctt gct aaa aag gga gtc aat cca ggc aag cta gat gta gaa ggc 556
Ile Leu Ala Lys Lys Gly Val Asn Pro Gly Lys Leu Asp Val Glu Gly
          40                      45                      50                      55

```

```

aga tct gcc ttt cat gtt gtg gcc tca aag gga aat ctt gag tgt ttg 604
Arg Ser Ala Phe His Val Val Ala Ser Lys Gly Asn Leu Glu Cys Leu
          60                      65                      70

```

```

aat gcc atc ctc ata cat gga gtt gat att aca acc agt gac acc gca 652

```

Asn	Ala	Ile	Leu	Ile	His	Gly	Val	Asp	Ile	Thr	Thr	Ser	Asp	Thr	Ala		
			75					80					85				
gga	agg	aat	gct	ctt	cac	ctg	gct	gca	aag	tat	ggg	cat	gca	ctg	tgt	700	
Gly	Arg	Asn	Ala	Leu	His	Leu	Ala	Ala	Lys	Tyr	Gly	His	Ala	Leu	Cys		
		90					95					100					
cta	caa	aaa	ctt	cta	cag	tac	aat	tgt	ccc	act	gaa	cat	gta	gac	ctg	748	
Leu	Gln	Lys	Leu	Leu	Gln	Tyr	Asn	Cys	Pro	Thr	Glu	His	Val	Asp	Leu		
	105					110					115						
cag	gga	aga	act	gca	ctt	cat	gat	gca	gct	atg	gca	gac	tgt	cct	tct	796	
Gln	Gly	Arg	Thr	Ala	Leu	His	Asp	Ala	Ala	Met	Ala	Asp	Cys	Pro	Ser		
120					125				130						135		
agc	ata	cag	ctg	ctc	tgc	gac	cat	ggg	gcc	tcg	gtg	aat	gcc	aaa	gat	844	
Ser	Ile	Gln	Leu	Leu	Cys	Asp	His	Gly	Ala	Ser	Val	Asn	Ala	Lys	Asp		
			140					145					150				
gta	gat	ggg	cgg	aca	cca	ctt	gtt	ctg	gct	acc	cag	atg	tgt	agg	cca	892	
Val	Asp	Gly	Arg	Thr	Pro	Leu	Val	Leu	Ala	Thr	Gln	Met	Cys	Arg	Pro		
		155						160					165				
aca	ata	tgt	caa	ctg	ctg	ata	gat	aga	ggg	gcg	gat	att	aat	tcc	aga	940	
Thr	Ile	Cys	Gln	Leu	Leu	Ile	Asp	Arg	Gly	Ala	Asp	Ile	Asn	Ser	Arg		
	170					175						180					
gac	aaa	caa	aac	agg	act	gct	ctc	atg	cta	gga	tgc	gag	tat	ggg	tgc	988	
Asp	Lys	Gln	Asn	Arg	Thr	Ala	Leu	Met	Leu	Gly	Cys	Glu	Tyr	Gly	Cys		
	185					190					195						
aaa	gat	gca	gta	gaa	gtc	tta	atc	aaa	aac	ggc	gct	gac	gtg	acc	ttg	1036	
Lys	Asp	Ala	Val	Glu	Val	Leu	Ile	Lys	Asn	Gly	Ala	Asp	Val	Thr	Leu		
200					205					210					215		
ctg	gac	gcc	ctt	ggc	cat	gac	agt	tct	tac	tat	gca	aga	att	ggg	gac	1084	
Leu	Asp	Ala	Leu	Gly	His	Asp	Ser	Ser	Tyr	Tyr	Ala	Arg	Ile	Gly	Asp		
			220						225					230			
aat	ctg	gac	att	cta	acc	tta	ctg	aag	act	gca	tca	gaa	aat	tcc	aac	1132	
Asn	Leu	Asp	Ile	Leu	Thr	Leu	Leu	Lys	Thr	Ala	Ser	Glu	Asn	Ser	Asn		
		235						240					245				
aaa	ggg	aga	gaa	ctt	tgg	aag	aaa	gga	cca	tct	tta	caa	cag	cga	aat	1180	
Lys	Gly	Arg	Glu	Leu	Trp	Lys	Lys	Gly	Pro	Ser	Leu	Gln	Gln	Arg	Asn		
	250					255						260					
ttg	tct	cag	atg	cta	gat	gaa	gta	aat	acg	aag	tca	aat	cag	agg	gag	1228	
Leu	Ser	Gln	Met	Leu	Asp	Glu	Val	Asn	Thr	Lys	Ser	Asn	Gln	Arg	Glu		
	265				270						275						
cat	caa	aac	att	cag	gat	ctg	gag	att	gaa	aat	gaa	gat	ctg	aaa	gag	1276	
His	Gln	Asn	Ile	Gln	Asp	Leu	Glu	Ile	Glu	Asn	Glu	Asp	Leu	Lys	Glu		
280					285				290						295		
aga	ttg	aga	aaa	att	cag	caa	gaa	cag	aga	ata	tta	ttg	gat	aaa	gtc	1324	
Arg	Leu	Arg	Lys	Ile	Gln	Gln	Glu	Gln	Arg	Ile	Leu	Leu	Asp	Lys	Val		
			300					305						310			
aat	ggg	tta	cag	cta	cag	ctg	aat	gag	gaa	gta	atg	gtg	gct	gat	gat	1372	
Asn	Gly	Leu	Gln	Leu	Gln	Leu	Asn	Glu	Glu	Val	Met	Val	Ala	Asp	Asp		

315	320	325	
ctg gaa agt gag aaa gaa aag	ctg aag tcc ctt ttg	gca gcc aaa gaa	1420
Leu Glu Ser Glu Lys Glu Lys	Leu Lys Ser Leu Leu	Ala Ala Lys Glu	
330	335	340	
aag cag cat gaa gaa agc cta	aga act att gag gct	ctg aaa agt aga	1468
Lys Gln His Glu Glu Ser	Leu Arg Thr Ile Glu	Ala Leu Lys Ser Arg	
345	350	355	
ttt aag tat ttt gag agt gat	cat tta gga tca gga	agt cat ttc agg	1516
Phe Lys Tyr Phe Glu Ser Asp	His Leu Gly Ser Gly	Ser His Phe Arg	
360	365	370	375
aaa gaa gat atg ctt ctt aaa	caa ggt caa atg tac	atg aca gac tca	1564
Lys Glu Asp Met	Leu Leu Lys Gln Gly	Gln Met Tyr Met Thr Asp Ser	
380	385	390	
cag tgt act tcc aca ggc atg	cca gtc cat atg caa	agc cga tct atg	1612
Gln Cys Thr Ser Thr Gly Met	Pro Val His Met Gln	Ser Arg Ser Met	
395	400	405	
tta aga cca ctg gag cta gcc	tta cct aat caa gcc	tca tat tcg gaa	1660
Leu Arg Pro Leu Glu Leu Ala	Leu Pro Asn Gln Ala	Ser Tyr Ser Glu	
410	415	420	
aac gaa att tta aag aaa gaa	tta gaa gca atg aga	act ttc tgt gat	1708
Asn Glu Ile Leu Lys Lys Glu	Leu Glu Ala Met Arg	Thr Phe Cys Asp	
425	430	435	
tca gca aaa caa gac aga ctc	aaa ctc caa aat gaa	ctg gct cac aag	1756
Ser Ala Lys Gln Asp Arg Leu	Lys Leu Gln Asn Glu	Leu Ala His Lys	
440	445	450	455
gtg gcg gag tgc aag gcc tta	gca ttg gaa tgt gaa	agg gtg aaa gag	1804
Val Ala Glu Cys Lys Ala Leu	Ala Leu Glu Cys Glu	Arg Val Lys Glu	
460	465	470	
gat tca gat gag cag ata aag	caa cta gaa gat gcc	ttg aaa gac gtg	1852
Asp Ser Asp Glu Gln Ile Lys	Gln Leu Glu Asp Ala	Leu Lys Asp Val	
475	480	485	
cag aag aga atg tat gag tcg	gaa ggt aaa gtg aaa	caa atg cag aca	1900
Gln Lys Arg Met Tyr Glu Ser	Glu Gly Lys Val Lys	Gln Met Gln Thr	
490	495	500	
cat ttt ctt gcc ttg aaa gag	cac ctg aca agt gat	gcg gcc act ggg	1948
His Phe Leu Ala Leu Lys Glu	His Leu Thr Ser Asp	Ala Ala Thr Gly	
505	510	515	
aac cac agg ctg atg gag gaa	ctg aag gat cag ttg	aaa gac atg aaa	1996
Asn His Arg Leu Met Glu Glu	Leu Lys Asp Gln Leu	Lys Asp Met Lys	
520	525	530	535
gtg aaa tac gaa ggt gcg tcc	gca gaa gtg ggg aaa	ttg aga aac caa	2044
Val Lys Tyr Glu Gly Ala Ser	Ala Glu Val Gly Lys	Leu Arg Asn Gln	
540	545	550	
atc aaa caa aat gaa atg tta	gtt gaa gag ttt aag	aga gat gag ggc	2092
Ile Lys Gln Asn Glu Met Leu	Val Glu Glu Phe Lys	Arg Asp Glu Gly	
555	560	565	

aag ctg atg gaa gag aat aag cga ctg cag aag gag ttg agc atg tgt Lys Leu Met Glu Glu Asn Lys Arg Leu Gln Lys Glu Leu Ser Met Cys 570 575 580	2140
gaa ctg gag cga gag aag aga gga agg aag ctc act gag atg gaa ggc Glu Leu Glu Arg Glu Lys Arg Gly Arg Lys Leu Thr Glu Met Glu Gly 585 590 595	2188
cag tta aag gac ttg tca gcc aag ctg gcc ctt tct att cca gca gag Gln Leu Lys Asp Leu Ser Ala Lys Leu Ala Leu Ser Ile Pro Ala Glu 600 605 610 615	2236
aaa ttt gaa aac atg aag agc ttg tta tca aat gaa ctg aac gag aag Lys Phe Glu Asn Met Lys Ser Leu Leu Ser Asn Glu Leu Asn Glu Lys 620 625 630	2284
gca aaa aaa tta ata gat gtg gaa aga gaa tat gaa aga tca ctt aat Ala Lys Lys Leu Ile Asp Val Glu Arg Glu Tyr Glu Arg Ser Leu Asn 635 640 645	2332
gaa act aga cca tta aag aga gaa ctt gag aat ttg aag gcc aaa ctg Glu Thr Arg Pro Leu Lys Arg Glu Leu Glu Asn Leu Lys Ala Lys Leu 650 655 660	2380
gct cag cac gtc aaa cca gag gaa cat gag cag ctc aag agc aga tta Ala Gln His Val Lys Pro Glu Glu His Glu Gln Leu Lys Ser Arg Leu 665 670 675	2428
gag cag aag tca gga gaa ctt ggg aag agg atc act gag tta aca tcg Glu Gln Lys Ser Gly Glu Leu Gly Lys Arg Ile Thr Glu Leu Thr Ser 680 685 690 695	2476
aaa aat cag acg tta caa aag gaa atc gaa aag gtc tgc ctg gat aat Lys Asn Gln Thr Leu Gln Lys Glu Ile Glu Lys Val Cys Leu Asp Asn 700 705 710	2524
aag ctc ctt aca caa caa gta aat aac tta aca act gaa atg aaa aat Lys Leu Leu Thr Gln Gln Val Asn Asn Leu Thr Thr Glu Met Lys Asn 715 720 725	2572
gtc cct tta aaa gta agt gaa gaa atg aaa aag tca cat gat gta att Val Pro Leu Lys Val Ser Glu Glu Met Lys Lys Ser His Asp Val Ile 730 735 740	2620
gtt gat gat ttg aat aaa aag ctt tca gat gtg aca cac aaa tat aca Val Asp Asp Leu Asn Lys Lys Leu Ser Asp Val Thr His Lys Tyr Thr 745 750 755	2668
gaa aag aag ttg gaa atg gag aag ttg ctt atg gaa aat gcc agt tta Glu Lys Lys Leu Glu Met Glu Lys Leu Leu Met Glu Asn Ala Ser Leu 760 765 770 775	2716
agt aaa aat gtc agc cgc ctg gaa act gtg ttc ata cct ccc gag aga Ser Lys Asn Val Ser Arg Leu Glu Thr Val Phe Ile Pro Pro Glu Arg 780 785 790	2764
cac gaa aaa gaa atg atg gct ctg aaa tcc aat atc act gaa ctt aag His Glu Lys Glu Met Met Ala Leu Lys Ser Asn Ile Thr Glu Leu Lys 795 800 805	2812

aag cag ctg tct gaa ctt aat aaa aaa tgt ggt gaa gac caa gag aaa 2860
Lys Gln Leu Ser Glu Leu Asn Lys Lys Cys Gly Glu Asp Gln Glu Lys
810 815 820

ata tat tca ctc atg tct gaa aac aat gat ttg aaa aag acc atg agt 2908
Ile Tyr Ser Leu Met Ser Glu Asn Asn Asp Leu Lys Lys Thr Met Ser
825 830 835

cat cag tat gtg ccc gtg aaa acc cat gaa gag att aaa act gcc ttg 2956
His Gln Tyr Val Pro Val Lys Thr His Glu Glu Ile Lys Thr Ala Leu
840 845 850 855

agt agc aca ttg gat aaa acc aat aga gaa tta gta gat gtg aag aag 3004
Ser Ser Thr Leu Asp Lys Thr Asn Arg Glu Leu Val Asp Val Lys Lys
860 865 870

aag tgt gaa gat ata aat caa gaa ttt gtg aaa ata aaa gat gag aac 3052
Lys Cys Glu Asp Ile Asn Gln Glu Phe Val Lys Ile Lys Asp Glu Asn
875 880 885

gaa ata tta aaa aga aat ctg gag aac act cag aac caa gta aaa gct 3100
Glu Ile Leu Lys Arg Asn Leu Glu Asn Thr Gln Asn Gln Val Lys Ala
890 895 900

gag tac atc agc cta aga gag cat gaa gaa aag atg agt ggc cta agg 3148
Glu Tyr Ile Ser Leu Arg Glu His Glu Glu Lys Met Ser Gly Leu Arg
905 910 915

aag agc atg aag aag gtc cag gac aac agc gct gaa ata ctg gct aag 3196
Lys Ser Met Lys Lys Val Gln Asp Asn Ser Ala Glu Ile Leu Ala Lys
920 925 930 935

tac aaa aaa agc cag gag gag att gtc acc ctg cat gag gag att gca 3244
Tyr Lys Lys Ser Gln Glu Glu Ile Val Thr Leu His Glu Glu Ile Ala
940 945 950

gcc cag aag aga gaa ctc gac acg ata cag gaa tgc atc aag cta aaa 3292
Ala Gln Lys Arg Glu Leu Asp Thr Ile Gln Glu Cys Ile Lys Leu Lys
955 960 965

tat gct ccg atc atc agc ttg gaa gag tgt gag aga aaa ttt aaa gcc 3340
Tyr Ala Pro Ile Ile Ser Leu Glu Glu Cys Glu Arg Lys Phe Lys Ala
970 975 980

act gag aaa gaa cta aaa gaa cag cta tcc cag cag aca cag aag tat 3388
Thr Glu Lys Glu Leu Lys Glu Gln Leu Ser Gln Gln Thr Gln Lys Tyr
985 990 995

aat acc agt gaa gaa gag gcc aag aag tgc aag caa gag aat gac aag 3436
Asn Thr Ser Glu Glu Glu Ala Lys Lys Cys Lys Gln Glu Asn Asp Lys
1000 1005 1010 1015

tta aag aag gag atc ctc act ctt cag aag gat cta aag gat aag aat 3484
Leu Lys Lys Glu Ile Leu Thr Leu Gln Lys Asp Leu Lys Asp Lys Asn
1020 1025 1030

gtt cac att gag aat tct tat gaa aca gaa aga gca tta agc aga aaa 3532
Val His Ile Glu Asn Ser Tyr Glu Thr Glu Arg Ala Leu Ser Arg Lys
1035 1040 1045

aca gaa gag ctg aac aga cag tta aaa gac ctg ttg cag aaa tac aca 3580

Thr	Glu	Glu	Leu	Asn	Arg	Gln	Leu	Lys	Asp	Leu	Leu	Gln	Lys	Tyr	Thr		
			1050				1055					1060					
gag	gca	aag	aag	gag	aaa	gag	aag	ctc	gtg	gag	gaa	aat	gcc	aag	cag	3628	
Glu	Ala	Lys	Lys	Glu	Lys	Glu	Lys	Leu	Val	Glu	Glu	Asn	Ala	Lys	Gln		
			1065				1070					1075					
act	tct	gag	atc	ctt	gca	gca	caa	act	ctt	ttg	cag	aag	cag	cat	gtt	3676	
Thr	Ser	Glu	Ile	Leu	Ala	Ala	Gln	Thr	Leu	Leu	Gln	Lys	Gln	His	Val		
					1085					1090					1095		
ccg	ctg	gag	cag	gtt	gag	tcc	ctg	aaa	aaa	tct	ctt	agt	ggt	aca	atc	3724	
Pro	Leu	Glu	Gln	Val	Glu	Ser	Leu	Lys	Lys	Ser	Leu	Ser	Gly	Thr	Ile		
				1100					1105						1110		
gag	aca	ctc	aag	gaa	gaa	ctg	aaa	act	aag	cag	aga	tgt	tat	gag	aaa	3772	
Glu	Thr	Leu	Lys	Glu	Glu	Leu	Lys	Thr	Lys	Gln	Arg	Cys	Tyr	Glu	Lys		
			1115					1120					1125				
gag	cag	cag	aca	gtg	acc	caa	ctg	cgg	cag	atg	ctg	gag	aat	cag	aag	3820	
Glu	Gln	Gln	Thr	Val	Thr	Gln	Leu	Arg	Gln	Met	Leu	Glu	Asn	Gln	Lys		
			1130				1135					1140					
aac	tcc	tct	gtg	ccc	ctg	gct	gag	cat	ttg	cag	gtt	aag	gaa	gca	ttt	3868	
Asn	Ser	Ser	Val	Pro	Leu	Ala	Glu	His	Leu	Gln	Val	Lys	Glu	Ala	Phe		
			1145			1150					1155						
gag	aaa	gaa	gtt	gga	atc	ata	aaa	gct	agc	ttg	aga	gaa	aag	gaa	gaa	3916	
Glu	Lys	Glu	Val	Gly	Ile	Ile	Lys	Ala	Ser	Leu	Arg	Glu	Lys	Glu	Glu		
			1160		1165				1170						1175		
gaa	agc	caa	aac	aaa	act	gaa	gag	gtc	tcc	aaa	ctc	cag	tct	gag	att	3964	
Glu	Ser	Gln	Asn	Lys	Thr	Glu	Glu	Val	Ser	Lys	Leu	Gln	Ser	Glu	Ile		
				1180					1185					1190			
cag	aat	act	aaa	caa	gcg	tta	aaa	aaa	tta	gag	act	cgg	gag	gtg	gtt	4012	
Gln	Asn	Thr	Lys	Gln	Ala	Leu	Lys	Lys	Leu	Glu	Thr	Arg	Glu	Val	Val		
			1195					1200					1205				
gat	ttg	tcg	aaa	tat	aaa	gca	acg	aaa	agc	gat	ttg	gag	aca	cag	att	4060	
Asp	Leu	Ser	Lys	Tyr	Lys	Ala	Thr	Lys	Ser	Asp	Leu	Glu	Thr	Gln	Ile		
			1210				1215					1220					
tcc	gac	tta	aac	gaa	aaa	ttg	gcc	aat	ctg	aat	agg	aag	tat	gag	gaa	4108	
Ser	Asp	Leu	Asn	Glu	Lys	Leu	Ala	Asn	Leu	Asn	Arg	Lys	Tyr	Glu	Glu		
			1225				1230				1235						
gta	tgt	gag	gag	gtt	ttg	cat	gcc	aaa	aag	aag	gaa	ctg	tct	gct	aaa	4156	
Val	Cys	Glu	Glu	Val	Leu	His	Ala	Lys	Lys	Lys	Glu	Leu	Ser	Ala	Lys		
					1245					1250					1255		
gat	gag	aag	gaa	ttg	ctc	cat	ttc	agc	ata	gag	caa	gaa	atc	aaa	gat	4204	
Asp	Glu	Lys	Glu	Leu	Leu	His	Phe	Ser	Ile	Glu	Gln	Glu	Ile	Lys	Asp		
				1260					1265					1270			
cag	cag	gaa	cga	tgt	gac	aaa	tcc	tta	aca	acc	atc	acg	gag	cta	cag	4252	
Gln	Gln	Glu	Arg	Cys	Asp	Lys	Ser	Leu	Thr	Thr	Ile	Thr	Glu	Leu	Gln		
			1275					1280					1285				
aga	aga	ata	cag	gaa	tct	gcc	aaa	caa	atc	gaa	gca	aaa	gat	aat	aag	4300	
Arg	Arg	Ile	Gln	Glu	Ser	Ala	Lys	Gln	Ile	Glu	Ala	Lys	Asp	Asn	Lys		

1290	1295	1300	
ata act gaa ctg ctc aat gat gtg gag aga tta aaa cag gcc ctc aat			4348
Ile Thr Glu Leu Leu Asn Asp Val Glu Arg Leu Lys Gln Ala Leu Asn			
1305	1310	1315	
ggc ctt tcc cag ctc acc tat gga agt ggg agt ccc agc aag agg cag			4396
Gly Leu Ser Gln Leu Thr Tyr Gly Ser Gly Ser Pro Ser Lys Arg Gln			
1320	1325	1330	1335
agt cag ctg att gac agc ctg cag cag cag gtc agg tcc ctg cag cag			4444
Ser Gln Leu Ile Asp Ser Leu Gln Gln Gln Val Arg Ser Leu Gln Gln			
1340	1345	1350	
cag ctg gcg gat gcc gac aga cag cac caa gaa gta att gca att tat			4492
Gln Leu Ala Asp Ala Asp Arg Gln His Gln Glu Val Ile Ala Ile Tyr			
1355	1360	1365	
cgg aca cac ctt ctt agt gct gca cag ggt cac atg gat gag gat gtg			4540
Arg Thr His Leu Leu Ser Ala Ala Gln Gly His Met Asp Glu Asp Val			
1370	1375	1380	
cag gcc gcc tta ctg cag atc ata cag atg cgg cag ggg ctc gtg tgc			4588
Gln Ala Ala Leu Leu Gln Ile Ile Gln Met Arg Gln Gly Leu Val Cys			
1385	1390	1395	
tag tcg gca cccccagcc cacagtggct ttccctgctg gtgctgagca			4637
* Ser Ala			
1400			
ttctgtgcgc aacttcatgg cctttctggg cctcgctgtg ctagtataat taaaataaag			4697
tgtattttga tccatcaaaa aaaaaaaaaa aaa			4730

<210> 2
 <211> 1401
 <212> PRT
 <213> Bos taurus

<400> 2

Met Met Ser Cys Trp Phe Ser Cys Ala Pro Lys Asn Arg Gln Ala Ala			
1	5	10	15
Asp Trp Asn Lys Tyr Asp Asp Arg Leu Met Arg Ala Ala Glu Arg Gly			
20	25	30	
Asp Val Glu Lys Val Ser Ser Ile Leu Ala Lys Lys Gly Val Asn Pro			
35	40	45	
Gly Lys Leu Asp Val Glu Gly Arg Ser Ala Phe His Val Val Ala Ser			
50	55	60	
Lys Gly Asn Leu Glu Cys Leu Asn Ala Ile Leu Ile His Gly Val Asp			
65	70	75	80
Ile Thr Thr Ser Asp Thr Ala Gly Arg Asn Ala Leu His Leu Ala Ala			
85	90	95	
Lys Tyr Gly His Ala Leu Cys Leu Gln Lys Leu Leu Gln Tyr Asn Cys			
100	105	110	
Pro Thr Glu His Val Asp Leu Gln Gly Arg Thr Ala Leu His Asp Ala			
115	120	125	
Ala Met Ala Asp Cys Pro Ser Ser Ile Gln Leu Leu Cys Asp His Gly			
130	135	140	
Ala Ser Val Asn Ala Lys Asp Val Asp Gly Arg Thr Pro Leu Val Leu			
145	150	155	160
Ala Thr Gln Met Cys Arg Pro Thr Ile Cys Gln Leu Leu Ile Asp Arg			
165	170	175	

Gly Ala Asp Ile Asn Ser Arg Asp Lys Gln Asn Arg Thr Ala Leu Met
 180 185 190
 Leu Gly Cys Glu Tyr Gly Cys Lys Asp Ala Val Glu Val Leu Ile Lys
 195 200 205
 Asn Gly Ala Asp Val Thr Leu Leu Asp Ala Leu Gly His Asp Ser Ser
 210 215 220
 Tyr Tyr Ala Arg Ile Gly Asp Asn Leu Asp Ile Leu Thr Leu Leu Lys
 225 230 235 240
 Thr Ala Ser Glu Asn Ser Asn Lys Gly Arg Glu Leu Trp Lys Lys Gly
 245 250 255
 Pro Ser Leu Gln Gln Arg Asn Leu Ser Gln Met Leu Asp Glu Val Asn
 260 265 270
 Thr Lys Ser Asn Gln Arg Glu His Gln Asn Ile Gln Asp Leu Glu Ile
 275 280 285
 Glu Asn Glu Asp Leu Lys Glu Arg Leu Arg Lys Ile Gln Gln Glu Gln
 290 295 300
 Arg Ile Leu Leu Asp Lys Val Asn Gly Leu Gln Leu Gln Leu Asn Glu
 305 310 315 320
 Glu Val Met Val Ala Asp Asp Leu Glu Ser Glu Lys Glu Lys Leu Lys
 325 330 335
 Ser Leu Leu Ala Ala Lys Glu Lys Gln His Glu Glu Ser Leu Arg Thr
 340 345 350
 Ile Glu Ala Leu Lys Ser Arg Phe Lys Tyr Phe Glu Ser Asp His Leu
 355 360 365
 Gly Ser Gly Ser His Phe Arg Lys Glu Asp Met Leu Leu Lys Gln Gly
 370 375 380
 Gln Met Tyr Met Thr Asp Ser Gln Cys Thr Ser Thr Gly Met Pro Val
 385 390 395 400
 His Met Gln Ser Arg Ser Met Leu Arg Pro Leu Glu Leu Ala Leu Pro
 405 410 415
 Asn Gln Ala Ser Tyr Ser Glu Asn Glu Ile Leu Lys Lys Glu Leu Glu
 420 425 430
 Ala Met Arg Thr Phe Cys Asp Ser Ala Lys Gln Asp Arg Leu Lys Leu
 435 440 445
 Gln Asn Glu Leu Ala His Lys Val Ala Glu Cys Lys Ala Leu Ala Leu
 450 455 460
 Glu Cys Glu Arg Val Lys Glu Asp Ser Asp Glu Gln Ile Lys Gln Leu
 465 470 475 480
 Glu Asp Ala Leu Lys Asp Val Gln Lys Arg Met Tyr Glu Ser Glu Gly
 485 490 495
 Lys Val Lys Gln Met Gln Thr His Phe Leu Ala Leu Lys Glu His Leu
 500 505 510
 Thr Ser Asp Ala Ala Thr Gly Asn His Arg Leu Met Glu Glu Leu Lys
 515 520 525
 Asp Gln Leu Lys Asp Met Lys Val Lys Tyr Glu Gly Ala Ser Ala Glu
 530 535 540
 Val Gly Lys Leu Arg Asn Gln Ile Lys Gln Asn Glu Met Leu Val Glu
 545 550 555 560
 Glu Phe Lys Arg Asp Glu Gly Lys Leu Met Glu Glu Asn Lys Arg Leu
 565 570 575
 Gln Lys Glu Leu Ser Met Cys Glu Leu Glu Arg Glu Lys Arg Gly Arg
 580 585 590
 Lys Leu Thr Glu Met Glu Gly Gln Leu Lys Asp Leu Ser Ala Lys Leu
 595 600 605
 Ala Leu Ser Ile Pro Ala Glu Lys Phe Glu Asn Met Lys Ser Leu Leu
 610 615 620
 Ser Asn Glu Leu Asn Glu Lys Ala Lys Lys Leu Ile Asp Val Glu Arg
 625 630 635 640
 Glu Tyr Glu Arg Ser Leu Asn Glu Thr Arg Pro Leu Lys Arg Glu Leu
 645 650 655
 Glu Asn Leu Lys Ala Lys Leu Ala Gln His Val Lys Pro Glu Glu His

										660						665						670									
Glu	Gln	Leu	Lys	Ser	Arg	Leu	Glu	Gln	Lys	Ser	Gly	Glu	Leu	Gly	Lys																
										675			680			685															
Arg	Ile	Thr	Glu	Leu	Thr	Ser	Lys	Asn	Gln	Thr	Leu	Gln	Lys	Glu	Ile																
										690			695			700															
Glu	Lys	Val	Cys	Leu	Asp	Asn	Lys	Leu	Leu	Thr	Gln	Gln	Val	Asn	Asn																
705											710			715			720														
Leu	Thr	Thr	Glu	Met	Lys	Asn	Val	Pro	Leu	Lys	Val	Ser	Glu	Glu	Met																
										725			730			735															
Lys	Lys	Ser	His	Asp	Val	Ile	Val	Asp	Asp	Leu	Asn	Lys	Lys	Leu	Ser																
										740			745			750															
Asp	Val	Thr	His	Lys	Tyr	Thr	Glu	Lys	Lys	Leu	Glu	Met	Glu	Lys	Leu																
										755			760			765															
Leu	Met	Glu	Asn	Ala	Ser	Leu	Ser	Lys	Asn	Val	Ser	Arg	Leu	Glu	Thr																
										770			775			780															
Val	Phe	Ile	Pro	Pro	Glu	Arg	His	Glu	Lys	Glu	Met	Met	Ala	Leu	Lys																
785											790			795			800														
Ser	Asn	Ile	Thr	Glu	Leu	Lys	Lys	Gln	Leu	Ser	Glu	Leu	Asn	Lys	Lys																
										805			810			815															
Cys	Gly	Glu	Asp	Gln	Glu	Lys	Ile	Tyr	Ser	Leu	Met	Ser	Glu	Asn	Asn																
										820			825			830															
Asp	Leu	Lys	Lys	Thr	Met	Ser	His	Gln	Tyr	Val	Pro	Val	Lys	Thr	His																
										835			840			845															
Glu	Glu	Ile	Lys	Thr	Ala	Leu	Ser	Ser	Thr	Leu	Asp	Lys	Thr	Asn	Arg																
										850			855			860															
Glu	Leu	Val	Asp	Val	Lys	Lys	Cys	Glu	Asp	Ile	Asn	Gln	Glu	Phe																	
865											870			875			880														
Val	Lys	Ile	Lys	Asp	Glu	Asn	Glu	Ile	Leu	Lys	Arg	Asn	Leu	Glu	Asn																
										885			890			895															
Thr	Gln	Asn	Gln	Val	Lys	Ala	Glu	Tyr	Ile	Ser	Leu	Arg	Glu	His	Glu																
										900			905			910															
Glu	Lys	Met	Ser	Gly	Leu	Arg	Lys	Ser	Met	Lys	Lys	Val	Gln	Asp	Asn																
										915			920			925															
Ser	Ala	Glu	Ile	Leu	Ala	Lys	Tyr	Lys	Lys	Ser	Gln	Glu	Glu	Ile	Val																
										930			935			940															
Thr	Leu	His	Glu	Glu	Ile	Ala	Ala	Gln	Lys	Arg	Glu	Leu	Asp	Thr	Ile																
945											950			955			960														
Gln	Glu	Cys	Ile	Lys	Leu	Lys	Tyr	Ala	Pro	Ile	Ile	Ser	Leu	Glu	Glu																
										965			970			975															
Cys	Glu	Arg	Lys	Phe	Lys	Ala	Thr	Glu	Lys	Glu	Leu	Lys	Glu	Gln	Leu																
										980			985			990															
Ser	Gln	Gln	Thr	Gln	Lys	Tyr	Asn	Thr	Ser	Glu	Glu	Glu	Ala	Lys	Lys																
										995			1000			1005															
Cys	Lys	Gln	Glu	Asn	Asp	Lys	Leu	Lys	Lys	Glu	Ile	Leu	Thr	Leu	Gln																
										1010			1015			1020															
Lys	Asp	Leu	Lys	Asp	Lys	Asn	Val	His	Ile	Glu	Asn	Ser	Tyr	Glu	Thr																
										1025			1030			1035															
Glu	Arg	Ala	Leu	Ser	Arg	Lys	Thr	Glu	Glu	Leu	Asn	Arg	Gln	Leu	Lys																
										1045			1050			1055															
Asp	Leu	Leu	Gln	Lys	Tyr	Thr	Glu	Ala	Lys	Lys	Glu	Lys	Glu	Lys	Leu																
										1060			1065			1070															
Val	Glu	Glu	Asn	Ala	Lys	Gln	Thr	Ser	Glu	Ile	Leu	Ala	Ala	Gln	Thr																
										1075			1080			1085															
Leu	Leu	Gln	Lys	Gln	His	Val	Pro	Leu	Glu	Gln	Val	Glu	Ser	Leu	Lys																
										1090			1095			1100															
Lys	Ser	Leu	Ser	Gly	Thr	Ile	Glu	Thr	Leu	Lys	Glu	Glu	Leu	Lys	Thr																
										1105			1110			1115			1120												
Lys	Gln	Arg	Cys	Tyr	Glu	Lys	Glu	Gln	Gln	Thr	Val	Thr	Gln	Leu	Arg																
										1125			1130			1135															
Gln	Met	Leu	Glu	Asn	Gln	Lys	Asn	Ser	Ser	Val	Pro	Leu	Ala	Glu	His																
										1140			1145			1150															

Leu Gln Val Lys Glu Ala Phe Glu Lys Glu Val Gly Ile Ile Lys Ala
 1155 1160 1165
 Ser Leu Arg Glu Lys Glu Glu Glu Ser Gln Asn Lys Thr Glu Glu Val
 1170 1175 1180
 Ser Lys Leu Gln Ser Glu Ile Gln Asn Thr Lys Gln Ala Leu Lys Lys
 1185 1190 1195 1200
 Leu Glu Thr Arg Glu Val Val Asp Leu Ser Lys Tyr Lys Ala Thr Lys
 1205 1210 1215
 Ser Asp Leu Glu Thr Gln Ile Ser Asp Leu Asn Glu Lys Leu Ala Asn
 1220 1225 1230
 Leu Asn Arg Lys Tyr Glu Glu Val Cys Glu Glu Val Leu His Ala Lys
 1235 1240 1245
 Lys Lys Glu Leu Ser Ala Lys Asp Glu Lys Glu Leu Leu His Phe Ser
 1250 1255 1260
 Ile Glu Gln Glu Ile Lys Asp Gln Gln Glu Arg Cys Asp Lys Ser Leu
 1265 1270 1275 1280
 Thr Thr Ile Thr Glu Leu Gln Arg Arg Ile Gln Glu Ser Ala Lys Gln
 1285 1290 1295
 Ile Glu Ala Lys Asp Asn Lys Ile Thr Glu Leu Leu Asn Asp Val Glu
 1300 1305 1310
 Arg Leu Lys Gln Ala Leu Asn Gly Leu Ser Gln Leu Thr Tyr Gly Ser
 1315 1320 1325
 Gly Ser Pro Ser Lys Arg Gln Ser Gln Leu Ile Asp Ser Leu Gln Gln
 1330 1335 1340
 Gln Val Arg Ser Leu Gln Gln Gln Leu Ala Asp Ala Asp Arg Gln His
 1345 1350 1355 1360
 Gln Glu Val Ile Ala Ile Tyr Arg Thr His Leu Leu Ser Ala Ala Gln
 1365 1370 1375
 Gly His Met Asp Glu Asp Val Gln Ala Ala Leu Leu Gln Ile Ile Gln
 1380 1385 1390
 Met Arg Gln Gly Leu Val Cys Ser Ala
 1395 1400

<210> 3
 <211> 4206
 <212> DNA
 <213> Bos taurus

<400> 3
 atgatgagct gttggttttc ttgtgctcct aagaacagac aagcagcaga ttggaacaaa 60
 tacgatgacc gattgatgag agcagcagaa aggggagatg tagaaaaagt gtcctcaatc 120
 cttgctaaaa agggagtcaa tccaggcaag ctagatgtag aaggcagatc tgcctttcat 180
 gttgtggcct caaagggaaa tcttgagtgt ttgaatgcc aacctcataca tggagttgat 240
 attacaacca gtgacaccgc aggaaggaat gctcttcacc tggctgcaaa gtatgggcat 300
 gcaactgtgtc tacaaaaact tctacagtac aattgtccca ctgaacatgt agacctgcag 360
 ggaagaactg cacttcatga tgcagctatg gcagactgtc cttctagcat acagctgctc 420
 tgcgaccatg gggcctcggt gaatgccaaa gatgtagatg ggcggacacc acttgttctg 480
 gctaccagag tgtgtaggcc aacaatatgt caactgctga tagatagagg ggcggatatt 540
 aattccagag acaaacaaaa caggactgct ctcagtctag gatgagagta tgggtgcaaa 600
 gatgcagtag aagtcttaat caaaaacggc gctgacgtga ctttgctgga cgcccttggc 660
 catgacagtt cttactatgc aagaattggt gacaatctgg acattctaac cttactgaag 720
 actgcatcag aaaattccaa caaagggaga gaactttgga agaaaggacc atctttacaa 780
 cagcgaaatt tgtctcagat gctagatgaa gtaaatacga agtcaaata gagggagcat 840
 caaacattc aggatctgga gattgaaaat gaagatctga aagagagatt gagaaaaatt 900
 cagcaagaac agagaatatt attggataaa gtcaatgggt tacagctaca gctgaatgag 960
 gaagtaatgg tggctgatga tctggaaaagt gagaaagaaa agctgaagtc ctttttggca 1020
 gccaaagaaa agcagcatga agaaagccta agaactattg aggctctgaa aagtagattt 1080
 aagtattttg agagtgatca tttaggatca ggaagtcatt tcaggaaaga agatatgctt 1140
 cttaaacaag gtcaaatgta catgacagac tcacagtgt cttccacagg catgccagtc 1200
 catatgcaaa gccgatctat gttaagacca ctggagctag ctttacctaa tcaagcctca 1260

tattcggaaa	acgaaattttt	aaagaaagaa	ttagaagcaa	tgagaacttt	ctgtgattca	1320
gcaaaacaag	acagactcaa	actccaaaat	gaactggctc	acaaggtggc	ggagtgcag	1380
gccttagcat	tggaatgtga	aagggtgaaa	gaggattcag	atgagcagat	aaagcaacta	1440
gaagatgcct	tgaaagacgt	gcagaagaga	atgtatgagt	cggagggtaa	agtgaacaa	1500
atgcagacac	atcttcttgc	cttgaaagag	cacctgacaa	gtgatgcggc	caactgggaac	1560
cacaggctga	tggaggaact	gaaggatcag	ttgaaagaca	tgaaagtga	atacgaagg	1620
gcgtccgcag	aagtggggaa	attgagaaac	caaatacaac	aaaatgaaat	gttagttgaa	1680
gagtttaaga	gagatgaggg	caagctgatg	gaagagaata	agcgactgca	gaaggagttg	1740
agcatgtgtg	aactggagcg	agagaagaga	ggaagggaagc	tcactgagat	ggaaggccag	1800
ttaaaggact	tgtcagccaa	gctggccctt	tctattccag	cagagaaatt	tgaaaacatg	1860
aagagcttgt	tatcaaata	actgaacgag	aaggcaaaaa	aattaataga	tgtggaaaga	1920
gaatatgaaa	gatcacttaa	tgaaactaga	ccattaaaga	gagaacttga	gaatttgaag	1980
gccaaactgg	ctcagcacgt	caaaccagag	gaacatgagc	agctcaagag	cagatttagag	2040
cagaagtcag	gagaacttgg	gaagaggatc	actgagttaa	catcgaaaaa	tcagacgtta	2100
caaaaggaaa	tcgaaaagg	ctgcctggat	aaataagctcc	ttacacaaca	agtaataaac	2160
ttaacaactg	aaatgaaaaa	tgtcccttta	aaagtaagt	aagaaatgaa	aaagtcacat	2220
gatgtaattg	ttgatgattt	gaataaaaaa	ctttcagatg	tgacacacaa	atatacagaa	2280
aagaagtggg	aaatggagaa	ggtgcttatg	gaaaatgcc	gtttaagtaa	aaatgtcagc	2340
cgcttgaaa	ctgtgttcat	acctcccgag	agacacgaaa	aagaaatgat	ggctctgaaa	2400
tccaatatca	ctgaacttaa	gaagcagctg	tctgaactta	ataaaaaatg	tggtgaagac	2460
caagagaaaa	tatattcact	catgtctgaa	aacaatgatt	tgaaaaagac	catgagtcac	2520
cagtatgtgc	ccgtgaaaac	ccatgaagag	attaaaaactg	ccttgagtag	cacattggat	2580
aaaaccaata	gagaattagt	agatgtgaag	aagaagtgtg	aagatataaa	tcaagaattt	2640
gtgaaaataa	aagatgagaa	cgaaatatta	aaaagaaatc	tggagaacac	tcagaaccaa	2700
gtaaaagctg	agtacatcag	cctaagagag	catgaagaaa	agatgagtg	cctaagggaag	2760
agcatgaaga	aggccagga	caacagcgct	gaaataactgg	ctaagtacaa	aaaaagccag	2820
gaggagattg	tcaccctgca	tgaggagatt	gcagcccaga	agagagaact	cgacacgata	2880
caggaatgca	tcaagctaaa	atatgtctccg	atcatcagct	tggagagtg	tgagagaaaa	2940
tttaaagcca	ctgagaaaga	actaaaagaa	cagctatccc	agcagacaca	gaagtataat	3000
accagtgaag	aagaggccaa	gaagtgcag	caagagaatg	acaagttaaa	gaaggagatc	3060
ctcactcttc	agaaggatct	aaaggataag	aatgttcaca	ttgagaattc	ttatgaaaca	3120
gaaagagcat	taagcagaaa	aacagaagag	ctgaacagac	agttaaaaga	cctgttgag	3180
aaatacacag	aggcaaagaa	ggagaaagag	aagctcgtgg	aggaaaaatgc	caagcagact	3240
tctgagatcc	ttgcagcaca	aactcttttg	cagaagcagc	atgttccgct	ggagcaggtt	3300
gagtcctga	aaaaatctct	tagtggtaca	atcgagacac	tcaagggaaga	actgaaaact	3360
aagcagagat	gttatgagaa	agagcagcag	acagtgaccc	aactgcggca	gatgctggag	3420
aatcagaaga	actcctctgt	gcccctggct	gagcatttgc	aggttaaagga	agcatttgag	3480
aaagaagttg	gaatcataaa	agctagcttg	agagaaaagg	aagaagaaag	ccaaaacaaa	3540
actgaagagg	tctccaaact	ccagtctgag	attcagaata	ctaaacaagc	gttaaaaaaa	3600
ttagagactc	gggaggtgg	tgatttgtcg	aaataataag	caacgaaaag	cgatttgag	3660
acacagattt	ccgactttaa	cgaaaaattg	gccaatctga	atagggaagta	tgagggaagta	3720
tgtgaggagg	ttttgcatgc	caaaaaagaa	gaactgtctg	ctaaagatga	gaagggaattg	3780
ctccatttca	gcatagagca	agaaatcaaa	gatcagcagg	aacgatgtga	caaatacctta	3840
acaaccatca	cggagctaca	gagaagaata	caggaatctg	ccaaacaaat	cgaagcaaaa	3900
gataataaga	taactgaact	gctcaatgat	gtggagagat	taaaacaggc	cctcaatggc	3960
ctttcccgag	tcacctatgg	aagtgggag	cccagcaaga	ggcagagtca	gctgattgac	4020
agcctgcagc	agcaggctcag	gtccctgcag	cagcagctgg	cggatgccga	cagacagcac	4080
caagaagtaa	ttgcaattta	tcggacacac	cttcttagtg	ctgcacaggg	tcacatggat	4140
gaggatgtgc	aggccgcctt	actgcagatc	atacagatgc	ggcaggggct	cgtgtgctag	4200
tcggca						4206

<210> 4

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> Motif

<221> VARIANT

<222> 2, 7, 10-11, 13-15, 18, 19, 22, 23, 26, 27, 29, 30

<223> Xaa may be any amino acid

<221> VARIANT

<222> 4

<223> Xaa may be Pro or Ala

<221> VARIANT

<222> 16

<223> Xaa may be Val or Ile

<221> VARIANT

<222> 17

<223> Xaa may be Val or Ala

<221> VARIANT

<222> 31

<223> Xaa may be Thr or Asp

<400> 4

Gly	Xaa	Thr	Xaa	Leu	His	Xaa	Ala	Ala	Xaa	Xaa	Gly	Xaa	Xaa	Xaa	Xaa
1				5				10						15	
Xaa	Xaa	Xaa	Leu	Leu	Xaa	Xaa	Gly	Ala	Xaa	Xaa	Asn	Xaa	Xaa	Xaa	
			20					25					30		

<210> 5

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 5

gctctaattct gctcttgagc

20

<210> 6

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 6

ctagtcgact gttcctctgg tttgacgtg

29

<210> 7

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 7

tcagcctgtg gttccagtg g

21

<210> 8

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 8
tgtcaggtgc tctttcaagg c 21

<210> 9
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 9
gtagctgtaa accattgact 20

<210> 10
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 10
atattctctg ttcttgctga 20

<210> 11
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 11
ctagcttgcc tggattgact c 21

<210> 12
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 12
tttagcaagg attgaggaca c 21

<210> 13
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 13
cgggatcccc gtggaaagag aatatgaaag atca

34

<210> 14
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 14
cgggatcccc gcacacgagc ccctgccg

28

<210> 15
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 15
cgggatcccc aattcttatg aaacagaaag agca

34

<210> 16
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 16
cgggatcccc gcacacgagc ccctgccg

28

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 17
gaactggctc acaaggtggc

20

<210> 18
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 18
ggtgacaatc tggacattct aa

22

<210> 19
<211> 22

<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 19
tcctgtctat gatgagctgt tg 22

<210> 20
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 20
ggggtaccag tgttgaggcg gcaggat 27

<210> 21
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 21
gctctagact agtgatgggtg atgggtgatgg cacacgagcc cctgccg 47

<210> 22
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 22
ggaattcagt ggaaagagaa tatgaaaga 29

<210> 23
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 23
gcggatcctc aatgtgaaca ttc 23

<210> 24
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 24
cattgagaat tcttatgaaa cag

23

<210> 25
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 25
cgggatccaa ttcttatgaa acagaaagag

30